

# SEQUENCE LISTING

<110> Wyeth  
 Ling, Vincent  
 Carreno, Beatriz M.  
 Collins, Mary

<120> USE OF B7-H3 TO INHIBIT LYMPHOCYTE PROLIFERATION (As Amended)

<130> 08702.6108-00000

<140> US/10/824,481  
 <141> 2004-04-15

<160> 35

<170> PatentIn version 3.5

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Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu  
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn  
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala  
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe  
85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val  
100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp  
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys  
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Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr  
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val  
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Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr  
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu  
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn  
 210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln  
 225 230 235 240

Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser  
 245 250 255

Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg  
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Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln  
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Arg	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	Asn
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Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	Thr
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Glu	Gly	Arg	Asp	Gln	Gly	Ser	Ala	Tyr	Ser	Asn	Arg	Thr	Ala	Leu	Phe
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Pro	Asp	Leu	Leu	Val	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	Val
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Arg	Val	Thr	Asp	Glu	Gly	Ser	Tyr	Thr	Cys	Phe	Val	Ser	Ile	Gln	Asp
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Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asn	Met
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Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val  
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Phe Trp Lys Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr  
180 185 190

Ser Gln Met Ala Asn Glu Arg Gly Leu Phe Asp Val His Ser Val Leu  
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn  
210 215 220

Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln  
225 230 235 240

Pro Leu Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu Ser  
245 250 255

Val Cys Leu Val Val Leu Leu Val Ala Leu Ala Phe Val Cys Trp Arg  
260 265 270

Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln  
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Asp Gly Asp Gly Glu Gly Ser Lys Thr Ala Leu Arg Pro Leu Lys Pro  
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Ser Glu Asn Lys Glu Asp Asp Gly Gln Glu Ile Ala  
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Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu  
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn  
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala  
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe  
85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val  
100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp  
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys  
130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr  
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val  
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr  
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu  
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn  
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Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln  
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Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val

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Ser	Phe	Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	
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Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	
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Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	Ser	
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Ser	Tyr	Arg	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	Gly	Gln	
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Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	Ala	Asn	Glu	
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Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	Val	Leu	Gly	Ala	
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Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	Val	Leu	Gln	Gln	Asp	
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Ala	His	Gly	Ser	Val	Thr	Ile	Thr	Gly	Gln	Pro	Met	Thr	Phe	Pro	Pro	
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Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	Ser	Val	Cys	Leu	Ile	Ala	Leu	
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Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys  
485 490 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly  
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Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp  
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Asp Gly Gln Glu Ile Ala  
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<213> Homo sapiens

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Thr Asp Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser  
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Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu  
35 40 45

Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn  
50 55 60

Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu  
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Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe  
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Leu	Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
		35					40					45			

Val	His	Ser	Phe	Xaa	Glu	Gly	Xaa	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	Asn
	50					55					60				

Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	Ser	Leu
65					70					75				80	

Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	Cys	Phe
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extracellular domain, Mus musculus IgG2am constant region chimera

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agaacactga accagtcctg gactctgatg gttcttactt catgtacagc aagctgagag	1560

tggaagaa gaactgggtg gaaagaaata gctactctg ttcagtggtc cactagggtc 1620

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<213> Artificial Sequence

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extracellular domain, Mus musculus IgG2am constant region chimera

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Leu Leu Phe Pro Ser Met Ala Ser Met Leu Glu Val Gln Val Pro Glu  
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Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Cys Cys Ser  
35 40 45

Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp  
50 55 60

Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala Glu Gly Gln  
65 70 75 80

Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu  
85 90 95

Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala  
100 105 110

Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser  
115 120 125

Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met  
130 135 140

Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile  
145 150 155 160

Thr Cys Ser Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln

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Asp	Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met				
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Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	Val				
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Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	Val	Leu				
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Gln	Gln	Asp	Ala	His	Gly	Ser	Val	Thr	Ile	Thr	Gly	Gln	Pro	Met	Thr				
225					230					235					240				
Phe	Pro	Pro	Glu	Ala	Gly	Ser	Gly	Ser	Glu	Pro	Arg	Gly	Pro	Thr	Ile				
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Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	Pro	Asn	Leu	Glu	Gly	Gly				
		260						265					270						
Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	Lys	Asp	Val	Leu	Met	Ile				
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Ala	Phe	Ala	Cys	Ala	Val	Asn	Asn	Lys	Asp	Leu	Pro	Ala	Pro	Ile	Glu				
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Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	Arg	Ala	Pro	Gln	Val	Tyr				
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Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	Gln	Val	Thr	Leu				
385					390					395					400				

Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp  
405 410 415

Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val  
420 425 430

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu  
435 440 445

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His  
450 455 460

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro  
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Gly Lys

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extracellular domain, Mus musculus IgG2am constant region chimera

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accgatgcca ccctgtgctg ctccttctcc cctgagcctg gcttcagcct ggcacagctc 180  
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gaccagggca ggcctatgc caaccgcacg gccctcttcc cggacctgct ggcacagggc 300  
aacgcatccc tgaggctgca gcgcgtgcgt gtggcggacg agggcagctt cacctgcttc 360  
gtgagcatcc gggatttcgg cagcgtgcc gtcagcctgc aggtggccgc tccctactcg 420  
aagcccagca tgaccctgga gcccaacaag gacctgcggc caggggacac ggtgaccatc 480  
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gtgcacagca tcctgcgggt ggtgctgggt gcaaattggc cctacagctg cctggtgcgc 660

aaccccggtgc tgcagcagga tgcgcacagc tctgtcacca tcacacccca gagaagcccc	720
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ctgactggca acgtgaccac gtcgcagatg gccaacgagc agggcttggt tgatgtgcac	1260
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aacatccctg cactagagga taagccatgt acagatccat ttccatctct cctcatcagc	1560
acctaacctc gaggggtggac catccgtctt catcttccct ccaaagatca aggatgtact	1620
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cagaagaaga gatgactaag aaacaggcca ctctgacctg catggtcaca gacttcatgc	2100
ctgaagacat ttacgtggag tggaccaaca acgggaaaac agagctaaac tacaagaaca	2160
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agaagaactg ggtggaaaga aatagctact cctgttcagt ggtccacgag ggtctgcaca	2280
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 extracellular domain, Mus musculus IgG2am constant region chimera  
  
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Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu Cys Cys Ser  
 35 40 45

Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp  
 50 55 60

Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala Glu Gly Gln  
 65 70 75 80

Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu  
 85 90 95

Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala  
 100 105 110

Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser  
 115 120 125

Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met  
 130 135 140

Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile  
 145 150 155 160

Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln  
 165 170 175

Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met



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Gln	Gln	Asp	Ala	His	Ser	Ser	Val	Thr	Ile	Thr	Pro	Gln	Arg	Ser	Pro
225					230					235					240
Thr	Gly	Ala	Val	Glu	Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu
				245					250					255	
Val	Gly	Thr	Asp	Ala	Thr	Leu	Arg	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly
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Phe	Ser	Leu	Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys
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Ala	Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala
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Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr
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Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln
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Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys
		355					360					365			
Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	Ser	Ser	Tyr	Arg
	370					375					380				
Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	Gly	Gln	Gly	Val	Pro
385					390					395					400
Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	Ala	Asn	Glu	Gln	Gly	Leu
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Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala Asn Gly Thr  
420 425 430

Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp Ala His Gly  
435 440 445

Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro Glu Ala Gly  
450 455 460

Ser Gly Ser Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys  
465 470 475 480

Lys Cys Pro Ala Pro Asn Leu Glu Gly Gly Pro Ser Val Phe Ile Phe  
485 490 495

Pro Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val  
500 505 510

Thr Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile  
515 520 525

Ser Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr  
530 535 540

His Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro  
545 550 555 560

Ile Gln His Gln Asp Trp Met Ser Gly Lys Ala Phe Ala Cys Ala Val  
565 570 575

Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro  
580 585 590

Lys Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu  
595 600 605

Glu Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp  
610 615 620

Phe Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr  
625 630 635 640

Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser  
645 650 655

Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu  
660 665 670

Arg Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His  
675 680 685

His Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
690 695 700

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acggatgcca ccctacgctg ctctttttcc ccagagcctg gcttcagtct ggcacagctc 180  
aacctcatct ggcagctgac agacaccaaa cagctggtgc acagcttcac ggagggccgg 240  
gaccaaggca gtgcctactc caaccgcaca gcgctcttcc ctgacctgtt ggtgcaaggc 300  
aatgcgtcct tgaggctgca gcgcgtccga gtaaccgacg agggcagcta cacctgcttt 360  
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gtgcccttga ctggcaatgt gaccacatcc cagatggcca acgagcgggg cttgttcgat 600  
gttcacagcg tgctgagggg ggtgctgggt gctaacggca cctacagctg cctggtacgc 660  
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gctataaaca tccctgcaact agaggataag ccatgtacag atccatttcc atctctctc 900  
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tgaccagat gtccagatca gctggtttgt gaacaacgtg gaagtacaca cagctcagac	1080
acaaacccat agagaggatt acaacagtac tctccgggtg gtcagtgcc tccccatcca	1140
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agaacactga accagtctct gactctgatg gttcttactt catgtacagc aagctgagag	1560
tggaaaagaa gaactgggtg gaaagaaata gctactcttg ttacgtggtc cactgagggtc	1620
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<400> 14

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Leu Leu Phe Pro Ser Met Ala Ser Met Val Glu Val Gln Val Ser Glu	
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Asp Pro Val Val Ala Leu Val Asp Thr Asp Ala Thr Leu Arg Cys Ser	
35 40 45	

Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp	
50 55 60	

Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg	
65 70 75 80	

Asp Gln Gly Ser Ala Tyr Ser Asn Arg Thr Ala Leu Phe Pro Asp Leu	
85 90 95	

Leu Val Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Thr	
100 105 110	

Asp Glu Gly Ser Tyr Thr Cys Phe Val Ser Ile Gln Asp Phe Asp Ser  
115 120 125

Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met  
130 135 140

Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asn Met Val Thr Ile  
145 150 155 160

Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val Phe Trp Lys  
165 170 175

Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met  
180 185 190

Ala Asn Glu Arg Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val  
195 200 205

Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu  
210 215 220

Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Leu Thr  
225 230 235 240

Phe Pro Pro Glu Ala Gly Ser Gly Ser Glu Pro Arg Gly Pro Thr Ile  
245 250 255

Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn Leu Glu Gly Gly  
260 265 270

Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp Val Leu Met Ile  
275 280 285

Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp Val Ser Glu Asp  
290 295 300

Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn Val Glu Val His  
305 310 315 320

Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn Ser Thr Leu Arg  
325 330 335

Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp Met Ser Gly Lys  
340 345 350

Ala Phe Ala Cys Ala Val Asn Asn Lys Asp Leu Pro Ala Pro Ile Glu  
355 360 365

Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala Pro Gln Val Tyr  
370 375 380

Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys Gln Val Thr Leu  
385 390 395 400

Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile Tyr Val Glu Trp  
405 410 415

Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn Thr Glu Pro Val  
420 425 430

Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys Leu Arg Val Glu  
435 440 445

Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys Ser Val Val His  
450 455 460

Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe Ser Arg Thr Pro  
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Gly Lys

<210> 15  
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<223> ALE, or another amino acid sequence

<220>  
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<222> (7)..(17)

<223> PEDPVVALVGT, or another amino acid sequence  
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 <222> (26)..(27)  
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 <223> FAEGQDQGSAY, or another amino acid sequence  
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 <222> (67)..(79)  
 <223> ALFPDLLAQGNAS, or another amino acid sequence  
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 <223> RVADEGSFTCFVSIRDF, or another amino acid sequence  
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 <222> (107)..(107)  
 <223> V, or another amino acid sequence

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Xaa	Asp	Ala	Thr	Leu	Cys	Cys	Ser	Phe	Xaa	Xaa	Glu	Pro	Gly	Phe	Ser
			20					25					30		

Leu	Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
		35					40				45				

Val	His	Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ala	Asn
	50					55					60				

Arg	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu
65					70				75						80

Arg	Leu	Gln	Arg	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85					90					95	

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Gly	Ser	Ala	Ala	Xaa	Ser	Leu	Gln	Val	Ala
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<220>  
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Val Gln Val  
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<210> 17  
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<220>  
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Asp Ala Thr Leu Cys Cys Ser Phe  
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<210> 18  
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<212> PRT  
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<220>  
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Asp Thr Lys Gln Leu Val His Ser  
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<210> 19  
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<212> PRT  
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Ala Asn Arg Thr



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<212> PRT  
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<220>  
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Leu Arg Leu Gln Arg Val  
1 5

<210> 21  
<211> 4  
<212> PRT  
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<220>  
<223> Conserved region in the Ig V-like domain(s) of mammalian B7-H3  
  
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Gly Ser Ala Ala  
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<210> 22  
<211> 5  
<212> PRT  
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<220>  
<223> Conserved region in the Ig V-like domain(s) of mammalian B7-H3  
  
<400> 22

Ser Leu Gln Val Ala  
1 5

<210> 23  
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<212> PRT  
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<222> (2) .. (2)

<223> L or V, or another amino acid

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<222> (22)..(22)

<223> C or R, or another amino acid

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<222> (53)..(53)

<223> A or T, or another amino acid

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<222> (56)..(56)

<223> Q or R, or another amino acid

<400> 23

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Thr	Asp	Ala	Thr	Leu	Xaa	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser
			20					25					30		

Leu	Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
		35					40					45			

Val	His	Ser	Phe	Xaa	Glu	Gly	Xaa	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	Asn
	50					55					60				

Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	Ser	Leu
65					70					75					80

Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	Cys	Phe
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Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala
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<211> 55

<212> DNA

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<220>

<223> Primer

<400> 24

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<220>  
<223> Primer

<400> 25  
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<210> 26  
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<212> DNA  
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<220>  
<223> Primer

<400> 26  
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<210> 27  
<211> 55  
<212> DNA  
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<220>

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21

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<212> DNA

<213> Artificial sequence

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<400> 35

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22